

modified residue is the first amino acid. For casein kinase II phosphorylation sites, the actual modified residue is the first amino acid. For the tyrosine kinase phosphorylation site, the actual modified residue is the last amino acid residue. For N-myristoylation sites, the actual modified residue is the first amino acid. In addition, a sulfatase signature is found from about amino acids 85-97.

On page 8, please replace paragraph 7 (lines 28-29) with the following paragraph:

Figure 10A and 10B shows the 25278 sulfatase cDNA sequence (SEQ ID NO:6) and the deduced amino acid sequence (SEQ ID NO:5).

On page 9, please replace paragraph 4 (lines 21-22) with the following paragraph:

Figure 15A and 15B shows the 26212 sulfatase cDNA sequence (SEQ ID NO:8) and the deduced amino acid sequence (SEQ ID NO:7).

On page 9, please replace paragraph 7 (beginning at line 29 and continuing to page 10, lines 1-6) with the following paragraph:

Figure 18A and 18B shows an analysis of the 26212 sulfatase open reading frame for amino acids corresponding to specific functional sites. For the N-glycosylation sites, the actual modified residue is the first amino acid. For cAMP- and cGMP-dependent protein kinase phosphorylation sites, the actual modified residue is the last amino acid. For protein kinase C phosphorylation sites, the actual modified residue is the first amino acid. For casein kinase II phosphorylation sites, the actual modified residue is the first amino acid. For the tyrosine kinase phosphorylation site, the actual modified residue is the last amino acid residue. For N-myristoylation sites, the actual modified residue is the first amino acid. In addition, sulfatase signature sites are found from about amino acids 168-177 and 120-132.